

IMMUNEX CORPORATION

Attorney Docket No. 2852-A

SEQUENCE LISTING

- (1) GENERAL INFORMATION:

10 (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF- κ B

(iii) NUMBER OF SEQUENCES: 19

15 (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Immunex Corporation, Law Department
- (B) STREET: 51 University Street
- (C) CITY: Seattle
- (D) STATE: WA
- (E) COUNTRY: USA
- (F) ZIP: 98101

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: Apple Power Macintosh
- (C) OPERATING SYSTEM: Apple Operating System 7.5.5
- (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

(vi) CURRENT APPLICATION DATA:

(VI) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
 (B) FILING DATE: 22 DECEMBER 1997
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: USSN 60/064,671
(B) FILING DATE: 14 OCTOBER 1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: USSN 08/813,509
(B) FILING DATE: 07 MARCH 1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

45 (A) APPLICATION NUMBER: USNN 08/772,330 (60/064,671)
(B) FILING DATE: 23 DECEMBER 1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

50 (A) NAME: Perkins, Patricia Anne
(B) REGISTRATION NUMBER: 34,693
(C) REFERENCE/DOCKET NUMBER: 2852-A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

60 (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 3115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
 (B) CLONE: 9D-8A

20

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 93..1868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGCTGCTG CTCTGCCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG 60

GAECTCTCTGC CTGACCTCAAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT
 Val Ala Leu Gln Ile Ala Pro 113

30

CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn 161
 10 15 20AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT
 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser 209
 25 30 35

35

GAC AGT GTA TGT CTG CCC TGT GGC CGG GAT GAA TAC TTG GAT AGC TGG
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp 257
 40 45 50 55AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys 305
 60 65 70GCC CTG GTG GCC GTG GTC GCC AAC AGC ACC CCC CGG CGC TGC
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys 353
 75 80 85GGC TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC
 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg 401
 90 95 100CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln 449
 105 110 115

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	CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser 120 125 130 135	497
5	GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr 140 145 150	545
10	TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala 155 160 165	593
15	GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His 170 175 180	641
20	GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala 185 190 195	689
25	CTG GTG GCT GCC ATC ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys 200 205 210 215	737
30	GCA CTC ACA GCT AAT TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg 220 225 230	785
35	CTA AGT GGA GAT AAG GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His 235 240 245	833
40	ACG GCA AAC TTT GGT CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu 250 255 260	881
45	ACT CTG GAG GAG AAG ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln 265 270 275	929
50	GGT GGT GTC TGT CAG GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln 280 285 290 295	977
55	GCC GAA GAT GCC AGG ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu 300 305 310	1025
60	GAA GAC AGC TTC AGA CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg 315 320 325	1073
	CCC TCC CAG CCC ACA GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser 330 335 340	1121
	AAA TCC ACA CCT CCT TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp 345 350 355	1169

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AGT TTA AGC CAG TGC TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA	1217
Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu	
360 365 370 375	

5 AGC TGC AAC TGC ACT GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG	1265
Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met	
380 385 390	

10 TCC TCT GAA AAC TAC TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG	1313
Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro	
395 400 405	

15 CAC TGG GCA GCC AGC CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC	1361
His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly	
410 415 420	

20 TGC CGG AAC CCT CCT GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA	1409
Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro	
425 430 435	

25 AAA CGT GGA CCC TTG CCC CAG TGC GCC TAT GGC ATG GGC CTT CCC CCT	1457
Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro	
440 445 450 455	

30 GAA GAA GAA GCC AGC AGG ACG GAG CCC AGA GAC CAG CCC GAG GAT GGG	1505
Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly	
460 465 470	

35 GCT GAT GGG AGG CTC CCA AGC TCA GCG AGG GCA GGT GCC GGG TCT GGA	1553
Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly	
475 480 485	

40 AGC TCC CCT GGT GGC CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC	1601
Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn	
490 495 500	

45 AGT AAC TCC ACG TTC ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC	1649
Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly	
505 510 515	

50 GAC ATC ATC GTG GTC TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG	1697
Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala	
520 525 530 535	

55 GCG GCT GCG GAG CCC ATG GGC CGC CCG GTG CAG GAG ACC CTG GCG	1745
Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala	
540 545 550	

60 CGC CGA GAC TCC TTC GCG GGG AAC GGC CCG CGC TTC CCG GAC CCG TGC	1793
Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys	
555 560 565	

65 GGC GGC CCC GAG GGG CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG	1841
Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val	
570 575 580	

70 CAG GAG CAA GGC GGG GCC AAG GCT TGA GCGCCCCCA TGGCTGGGAG	1888
Gln Glu Gln Gly Ala Lys Ala	
585 590	

75 CCCGAAGCTC GGAGGCCAGGG CTCGCGAGGG CAGCACCGCA GCCTCTGCC CAGCCCCGGC	1948
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RECEIVED
U.S. PATENT AND TRADEMARK OFFICE
JULY 10 1997

5	CACCCAGGG A TCGATCGTA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC	2008
	CTTCCAGGA ATGGGCTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCCACCGA	2068
	TGCTCACAG CCCGCCGCAC TGGGGCAGAT GTCTCCCTG CCACTCCCTCA AACTCGCAGC	2128
	AGTAATTGTG GGCACATATGA CAGCTATTT TATGACTATC CTGTTCTGTG GGGGGGGGT	2188
10	CTATGTTTC CCCCCATATT TGTATTCTT TTCATAACCTT TTCTTGATAT CTTTCTCCC	2248
	TCTTTTTAA TGTAAGGTT TTCTAAAAA TTCTCTAAA GGTTGAGGGTC TCTTTCTTT	2308
	CTCTTTCTT TTTTTTTGTC TTTTTTGCG AACCTGGCTC TGGCCCGAGC TAGAGTGCAG	2368
15	TGGTGCAGATT ATAGCCCCGT GCAGCCTCTA ACTCCTGGC TCAAGCAATC CAAGTGATCC	2428
	TCCCACCTCA ACCTTCGGAG TAGCTGGAT CACAGCTGCA GCCCACGCC AGCTTCCCTCC	2488
20	CCCCGACTCC CCCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAATC	2548
	CCCCAGCTAA AGCAGTCCTC CAGCCTGGC CTCCCAAAGT ACTGGGATTA CAGGCGTAG	2608
	CCCCCACGCT GGCTGCTTT ACGTATTITTC TTTTGTGCC CTGCTCACAG TGTTTTAGAG	2668
25	ATGGCTTCC CAGTGTGTG TCATTGTAAC CACTTTGGG AAAGGGCTAA ACATGTGAGG	2728
	CCTGGAGATA GTTGCTAAAGT TGCTAGAAC ATGTGGGGG ACTTTCATAT TCTGAAAAAT	2788
30	GTTCTATATT CTCATTTTC TAAAAGAAC AAAAAGGAA ACCCGATTTA TTCTCCTGA	2848
	ATCTTTTAA GTTGTGTCG TTCTTAAAGC AGAACTAACG TCAGTATGTG ACCTTACCCG	2908
	CTAGGTGGTT AATTATCCA TGCTGGCAGA GCCACTCAGG TACTTGGTAA GCAAATTCT	2968
35	AAAACCTCAA GTTGCTGCAG CTTGGCATTC TTCTTATTCT AGAGGTCTCT CTGGAAAAGA	3028
	TGGAGAAAAT GAACAGGACA TGGGGCTCT GGAAAGAAC GGCCCGGGAA GTTCAAGGAA	3088
40	GAATAAAGTT GAAATTAA AAAA	3115

(2) INFORMATION FOR SEQ ID NO:2:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- 50 (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

55	Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu	
	1 5 10 15	
	His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser	
	20 25 30	
60	Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro	
	35 40 45	

	Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His
	50 55 60
5	Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn
	65 70 75 80
	Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser
	85 90 95
10	Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu
	100 105 110
15	Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro
	115 120 125
	Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys
	130 135 140
20	Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His
	145 150 155 160
	Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg
	165 170 175
25	Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu
	180 185 190
	Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val
	195 200 205
	Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp
	210 215 220
35	Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly
	225 230 235 240
	Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala
	245 250 255
40	Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu
	260 265 270
	Asp Met Cys Tyr Pro Asp Gln Gly Val Cys Gln Gly Thr Cys Val
	275 280 285
	Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu
	290 295 300
50	Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr
	305 310 315 320
	Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu
	325 330 335
55	Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro
	340 345 350
	Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr
60	355 360 365

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Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys
370 375 380

5 Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu
385 390 395 400

Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn
405 410 415

10 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys
420 425 430

Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala
435 440 445

15 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala
450 455 460

20 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala
465 470 475 480

Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala
485 490 495

25 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly
500 505 510

Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln
515 520 525

30 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro
530 535 540

Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly
545 550 555 560

Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro
565 570 575

40 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala
580 585 590

(2) INFORMATION FOR SEQ ID NO:3:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

60 (vii) IMMEDIATE SOURCE:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
 (B) CLONE: 9D-15C

(ix) FEATURE:

5 (A) NAME/KEY: CDS
 (B) LOCATION: 39..1391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10	CCGCTGAGGC CGCGGCCGCC GCCAGCCTGT CCCCGGCC ATG GCC CCG CGC GCC Met Ala Pro Arg Ala	53
	1 5	
15	CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu	101
	10 15 20	
20	GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AST GAG Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu 25 30 35	149
25	AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro GLY 40 45 50	197
30	AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu 55 60 65	245
35	CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys 70 75 80 85	293
40	TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val 90 95 100	341
45	GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly 105 110 115	389
50	TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys 120 125 130	437
55	GCG CCG CGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr 135 140 145	485
60	GTG TGC AAA CCT TGC CTT GCA CGC TAC TTC TCT GAT GCC TTT TCC TCC Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Sér Ser 150 155 160 165	533
65	ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg 170 175 180	581
70	GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser 185 190 195	629

	CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro GLY 200 205 210	677
5	TTA ATA ATT CTG CTT CTC TTC CGC TCT GTG GCC CTG GTG GCT GCC ATC Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile 215 220 225	725
10	ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn 230 235 240 245	773
15	TG TG GAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys 250 255 260	821
20	GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC ACG GCA AAC TTT GGT Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe GLY 265 270 275	869
25	CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys 280 285 290	917
30	ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln 295 300 305	965
35	GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg 310 315 320 325	1013
40	ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg 330 335 340	1061
45	CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr 345 350 355	1109
50	GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro 360 365 370	1157
55	TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys 375 380 385	1205
60	TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr 390 395 400 405	1253
65	GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr 410 415 420	1301
70	TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser 425 430 435	1349

CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC
Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn
440 445 450

1391

5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
1 5 10 15

20 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
20 25 30

25 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
35 40 45

30 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser
50 55 60

35 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
65 70 75 80

40 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
85 90 95

45 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
100 105 110

50 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
115 120 125

55 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
130 135 140

60 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
145 150 155 160

65 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
165 170 175

70 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
180 185 190

75 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
195 200 205

80 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Phe Ala Ser Val Ala
210 215 220

85 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
225 230 235 240

Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
245 250 255

5 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
260 265 270

Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
275 280 285

10 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
290 295 300

Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln
305 310 315 320

15 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
325 330 335

20 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
340 345 350

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
355 360 365

25 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
370 375 380

30 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
385 390 395 400

Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
405 410 415

35 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
420 425 430

His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
435 440 445

40 Cys Arg Asn
450

45 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMO SAPIENS

60 (vii) IMMEDIATE SOURCE:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
 (B) CLONE: FULL LENGTH RANK

(ix) FEATURE:

5 (A) NAME/KEY: CDS
 (B) LOCATION: 39..1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10	CCGCTGAGGC CGCGGCCGCC GCCAGCTGT CCCCGGCC ATG GCC CCG CGC GCC Met Ala Pro Arg Ala	53
15	CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu	101
	10 15 20	
20	GCC CGG CTG CAG GTG CCT TTG CAG ATC GCT CCT CCA TGT ACC ACT GAG Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu	149
	25 30 35	
25	AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro GLY	197
	40 45 50	
30	AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu	245
	55 60 65	
35	CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys	293
	70 75 80 85	
40	TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val	341
	90 95 100	
45	GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly	389
	105 110 115	
50	TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys	437
	120 125 130	
55	GCG CGG CTG GGC GCC CAG CAC CGG TTG CAG CTC AAC AAG GAC ACA Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr	485
	135 140 145	
60	GTC TGC AAA CCT TGC CTT GCA CGC TAC TTC TCT GAT GCC TTT TCC TCC Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser	533
	150 155 160 165	
65	ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg	581
	170 175 180	
70	GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT CGC GTT TGC AGT TCT TCT Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser	629
	185 190 195	

	CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly 200 205 210	677
5	TTA ATA ATT CTG CTT CTC TTC CGG TCT GTG GCC CTG GTG GCT GCC ATC Leu Ile Ile Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile 215 220 225	725
10	ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn 230 235 240 245	773
15	TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys 250 255 260	821
20	GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC ACG GCA AAC TTT GGT Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly 265 270 275	869
25	CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys 280 285 290	917
30	ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Val Cys Gln 295 300 305	965
35	GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg 310 315 320 325	1013
40	ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Asp Ser Phe Arg 330 335 340	1061
45	CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr 345 350 355	1109
50	GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro 360 365 370	1157
55	TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA ACC CAG TGC Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys 375 380 385	1205
60	TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TAC Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr 390 395 400 405	1253
65	GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr 410 415 420	1301
70	TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser 425 430 435	1349

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	CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC CCT CCT Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro 440 445 450	1397
5	GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA AAA CGT GGA CCC TTG Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu 455 460 465	1445
10	CCC CAG TGC GCC TAT GGC ATG GGC CTT CCC CCT GAA GAA GAA GCC AGC Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser 470 475 480 485	1493
15	AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG GCT GAT GGG AGG CTC Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu 490 495 500	1541
20	CCA AGC TCA GCG AGG GCA GGT GCC GGG TCT GGA AGC TCC CCT GGT GGC Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly 505 510 515	1589
25	CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC AGT AAC TCC ACG TTC Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe 520 525 530	1637
30	ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC GAC ATC ATC GTG GTC Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val 535 540 545	1685
35	TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG GCT GCG GAG CCC Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro 550 555 560 565	1733
40	ATG GGC CGC CCG GTG CAG GAG GAC CTG GCG CGC CGA GAC TCC TTC Met Gly Arg Pro Val Gln Glu Thr Leu Ala Arg Arg Asp Ser Phe 570 575 580	1781
45	GCG GGG AAC GGC CCG CGC TTC CCG GAC CCG TGC GGC GGC CCC GAG GGG Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Pro Glu Gly 585 590 595	1829
50	CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG CAG GAG CAA GGC GGG Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly GLY 600 605 610	1877
55	GCC AAG GCT TGAGCGCCCC CCATGGCTGG GAGCCGAAG CTCGGAGCCA Ala Lys Ala 615	1926
60	GGGCTCGCGA GGGCAGCACCC GCAGCCCTTG CCCAGCCCC GGCCACCCAG GGATCGATCG GTACAGTCGA GGAAGACCAC CCGGCATTCT CTGCCACTT TGCTTCCAG GAAATGGGCT TTTCAGGAAG TGAATTGATG AGGACTGTCC CCATGCCAC GGATGCTCAG CAGCCCGCCG CACTGGGGCA GATGCTCCC CTGCCACTCC TCAAACCTCG AGCAGTAATT TGTGGCACTA TGACAGCTAT TTTTATGACT ATCCTGTTCT GTGGGGGGGG GGTCTATGTT TTCCCCCAT ATTGTATTC CTTTCATAA CTTTCTTGA TATCTTCTTCC CTCCTTTTT TAATGAAAG GTTTTCTCAA AAATTCTCCT AAAGGTGAGG GTCTCTTCTT TTCTCTTTT CTCCTTTTTT	1986 2046 2106 2166 2226 2286 2346

TTCTTTTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTCG ATTATAGCCC 2406
 5 GGTGCAGCCT CTAACCTCTG GGCTCAAGCA ATCCAAGTGA TCCTCCACC TCAACCTCG 2466
 GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTCC TCCCCCCAC TCCCCCC 2526
 10 CAGAGACACG GTCCACCAT GTTACCCAGC CTGGTCTCAA ACTCCCCAGC TAAAGCAGTC 2586
 15 CTCCAGCCTC GGCTCCCAA AGTACTGGGA TTACAGCGT GAGCCCCAC GCTGGCCTGC 2646
 TTTACGTATT TTCTTTGTG CCCCTGCTCA CAGTGTGTTA GAGATGGCTT TCCCAGTGTG 2706
 TGTTCATTGT AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA 2766
 20 AGTTGCTAGG AACATGTGGT GGGACTTCA TATTCTGAAA AATGTTCTAT ATTCTCATT 2826
 TTCTAAAGA AAGAAAAAG GAAACCAGT TTATTTCTCC TGAATCTTT TAAGTTGTG 2886
 25 TCGTTCTTA AGCAGAACTA AGCTCACTAT GTGACCTTAC CCCTAGGTG GTTAATTAT 2946
 CCATGCTGGC AGAGGCACTC AGGTACTTGG TAAGCAAATT TCTAAAACCT CAAGTTGCTG 3006
 30 CAGCTTGGCA TTCTTCTTAT TCTAGAGGT TCTCTGAAA AGATGGAGAA AATGAACAGG 3066
 35 ACATGGGGCT CCTGGGAAAAGA AAGGGCCCGG GAAGTTCAAG GAAGAATAAA GTTGAATTT 3126
 TAAAAAAAAA 3136

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 616 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
 1 5 10 15

Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
 20 25 30

Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
 35 40 45

Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser
 50 55 60

Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
 65 70 75 80

Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
 85 90 95

Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
 100 105 110

115 120 125

5 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
 130 135 140

Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
 145 150 155 160

10 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
 165 170 175

Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
 15 180 185 190

Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
 195 200 205

20 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
 210 215 220

Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
 225 230 235 240

25 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
 245 250 255

Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
 30 260 265 270

Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
 275 280 285

35 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
 290 295 300

Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln
 305 310 315 320

40 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
 325 330 335

Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
 45 340 345 350

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
 355 360 365

50 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
 370 375 380

Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
 385 390 395 400

55 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
 405 410 415

60 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
 420 425 430

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His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
435 440 445

5 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
450 455 460

Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
465 470 475 480

10 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
485 490 495

Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
500 505 510

15 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
515 520 525

20 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
530 535 540

Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
545 550 555 560

25 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
565 570 575

Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
580 585 590

30 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
595 600 605

35 Gln Glu Gln Gly Gly Ala Lys Ala
610 615

(2) INFORMATION FOR SEQ ID NO:7:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: FLAG® peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:8:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

5 (iii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

10 (vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc mutein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

20 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

25 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

30 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

35 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

40 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

45 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

50 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

55 Ser Leu Ser Leu Ser Pro Gly Lys
225 230

60 (2) INFORMATION FOR SEQ ID NO:9:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- 10 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: CMV (R2780 Leader)
- (ix) FEATURE:
(D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide;
Arg29 strengthens the furin cleavage site; nucleotides
encoding Thr30 and Ser31 add a SpeI site.
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr
1 5 10 15
- 25 Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser
20 25 30
- 30 (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 40 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus
- 45 (vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: RANKL
- 50 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..884
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CC GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro
60 1 5 10 15

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GCT CCG CGG CGG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu	95
20 25 30	25 30

5	CTG GGG CTG GGA CTG GGC CAG GTG TGC AGC ATC GCT CTG TTC CTG Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu	143
	35 40 45	35 40 45
10	TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr	191
	50 55 60	50 55 60
15	CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GAT TTG CAG His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln	239
	65 70 75	65 70 75
20	GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg	287
	80 85 90 95	80 85 90 95
25	ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile	335
	100 105 110	100 105 110
30	GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser	383
	115 120 125	115 120 125
35	TGG TTG GAT GTG GCC CAG CGA GGC CCT GAG GCC CAG CCA TTT GCA Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala	431
	130 135 140	130 135 140
40	CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val	479
	145 150 155	145 150 155
45	ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn	527
	160 165 170 175	160 165 170 175
50	ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr	575
	180 185 190	180 185 190
55	TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser	623
	195 200 205	195 200 205
60	GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser	671
	210 215 220	210 215 220
65	ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Ser Thr Lys	719
	225 230 235	225 230 235
70	AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly	767
	240 245 250 255	240 245 250 255

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GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC Gly Phe Phe Lys Leu Arg Ala Gly Glu Ile Ser Ile Gln Val Ser 260 265 270	815
5 AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 275 280 285	863
10 TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCTGTGGAAC ATTAGCATGG Phe Lys Val Gln Asp Ile Asp	914
15 ATGTCCCTAGA TGTTTGGAAA CTTCTAAAAA ATATGGATGAT GTCTATACAT GTGTAAGACT	974
20 ACTAAGAGAC ATGGCCCAAG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG GTGTTGTATA TGTAAGACTTAC ATAGGTGTGTT TAGATTCAT GGTGATTACA CAACGGTTT ACAATTTGT AATGATTCTTAC TAGAATTGAA CCAGATTGGG AGAGGTATTCC CGATGCTTAT	1034
25 GAAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA TGTGCCACTG AGAACCTTGA AATTAAAGAGG ATGCACATGTC ATTGCAAAGA AATGATAGTG	1094
30 TGAAGGGTTA AGTTCTTTG AATTGTATACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTT TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTCAG GTGTAATGTT TTCTGTGCAA AGTTTGAA ATTATATTG TGCTATAGTA TTTGATTCAA	1154
35 AATATTAA AATGTCCTCAC TGTGACATA TTTAATGTT TAAATGTACA GATGTATTAA ACTGGTGCAC TTTGTAATTCC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT	1214
40 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAC TTAATAGAGT CTTCAAG (2) INFORMATION FOR SEQ ID NO:11:	1274
45 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 amino acids (B) TYPE: amino acid (C) TOPOLOGY: linear	1334
50 (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	1394
55 Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala 1 5 10 15 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu 20 25 30	1454
60 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr 35 40 45 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His 50 55 60	1514
65	1574
70	1630

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Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp
65 70 75 80

5 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
85 90 95

Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
100 105 110

10 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
115 120 125

Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
130 135 140

15 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
145 150 155 160

Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
20 165 170 175

Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
180 185 190

25 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
195 200 205

Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
210 215 220

30 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
225 230 235 240

Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
35 245 250 255

Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
260 265 270

40 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
275 280 285

Lys Val Gln Asp Ile Asp
290

45

(2) INFORMATION FOR SEQ ID NO:12:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 954 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

60 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

5 (B) CLONE: huRANKL (full length)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..951

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15	ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG GAG Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu 1 5 10 15	48
20	GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC GCC Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala 20 25 30	96
25	CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC TCC CGC TCC ATG Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met 35 40 45	144
30	TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC GTC Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val 50 55 60	192
35	GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA TCA Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser 65 70 75 80	240
40	GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA AAT Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn 85 90 95	288
45	GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA ATA Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile 100 105 110	336
50	CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG CAA Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln 115 120 125	384
55	AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG AAA Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys 130 135 140	432
60	GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG CTT Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu 145 150 155 160	480
65	GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC CCA Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro 165 170 175	528
70	TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG GGT Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly 180 185 190	576

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TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA GTT
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205

5 AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA CAT
 Asn Gln Asp Gly Phe Tyr 210 215 220 His Arg His

10 CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG GTG
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240

15 TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG ATG
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255

AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT TTT
 Lys Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270

20 TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG GAA
 Tyr Ser Ile Asn Val Gly Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285

25 ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG GAT
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300

30 GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT TGA
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Ile Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:13:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

45 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1 5 10 15

Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30

50 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 55 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80

60 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
100 105 110

5 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130 135 140

10 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

15 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

20 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

25 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

30 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

35 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

40 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

45 (2) INFORMATION FOR SEQ ID NO:14:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1878 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Murine

5 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: Murine Fetal Liver Epithelium
 (B) CLONE: muRANK

10 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	GCC	CCG	CAG	CGC	CGG	CGG	CGC	CGC	CAG	CTG	CCC	GGG	CGG	CGG	CTG	CTG	48
Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Gln	Leu	Pro	Ala	Pro	Leu	Leu		
1				5					10						15		
GCG	CTC	TGC	GTG	CTG	CTC	GTT	CCA	CTG	CAG	GTG	ACT	CTC	CAG	GTC	ACT	96	
Ala	Ler	Cys	Val	Leu	Leu	Val	Pro	Leu	Gln	Val	Thr	Leu	Gln	Val	Thr		
				20				25				30					
CCT	CCA	TGC	ACC	CAG	GAG	AGG	CAT	TAT	GAG	CAT	CTC	GGG	CGG	TGT	TGC	144	
Pro	Pro	Cys	Thr	Gln	Glu	Arg	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys		
				35				40			45						
AGC	AGA	TGC	GAA	CCA	GGG	AAG	TAC	CTG	TCC	TCT	AAG	TGC	ACT	CCT	ACC	192	
Ser	Arg	Cys	Glu	Pro	Gly	Lys	Tyr	Leu	Ser	Ser	Lys	Cys	Thr	Pro	Thr		
				50				55			60						
TCC	GAC	AGT	GTG	TGT	CTG	CCC	TGT	GGC	CCC	GAT	GAG	TAC	TTG	GAC	ACC	240	
Ser	Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Thr		
				65				70			75			80			
TGG	AAT	GAA	GAA	GAT	AAA	TGC	TTG	CTG	CAT	AAA	GTC	TGT	GAT	GCA	GGC	288	
Trp	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Ala	Gly		
				85				90			95						
AAG	GCC	CTG	GTG	GCG	GTG	GAT	CCT	GGC	AAC	CAC	ACG	GCC	CGG	CGT	CGC	336	
Lys	Ala	Leu	Val	Ala	Val	Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg		
				100				105			110						
TGT	GCT	TGC	ACG	GCT	GGC	TAC	CAC	TGG	AAC	TCA	GAC	TGC	GAG	TGC	TGC	384	
Cys	A1a	Cys	Thr	A1a	Gly	Tyr	His	Trp	Asn	Ser	Asp	Cys	Glu	Cys	Cys		
				115				120			125						
CGC	AGG	AAC	ACG	GAG	TGT	GCA	CCT	GGC	TTC	GGG	GCT	CAG	CAT	CCC	TTG	432	
Arg	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu		
				130				135			140						
CAG	CTC	AAC	AAG	GAT	ACG	GTG	TGC	ACA	CCC	TGC	CTC	CTG	GGC	TTC	TTC	480	
Gln	Leu	Asn	Lys	Asp	Thr	Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe		
				145				150			155			160			
TCA	GAT	GTC	TTT	TCG	TCC	ACA	GAC	AAA	TGC	AAA	CCT	TGG	ACC	AAC	TGC	528	
Ser	Asp	Val	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys		
				165				170			175						
ACC	CTC	CTT	GGG	AAG	CTA	GAA	GCA	CAC	CAG	GGG	ACA	ACG	GAA	TCA	GAT	576	
Thr	Leu	Leu	Gly	Lys	Leu	Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp		
				180				185			190						

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GTC	GTC	TGC	AGC	TCT	TCC	ATG	ACA	CTG	AGG	AGA	CCA	CCC	AAG	GAG	GCC	624
Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	
195								200					205			

5	CAG	GCT	TAC	CTG	CCC	AGT	CTC	ATC	GTT	CTG	CTC	CTC	TTC	ATC	TCT	GTG	672
	Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	
	210						215					220					

10	GTA	GTA	GTG	GCT	ATC	ATC	TTC	GGC	GTT	TAC	TAC	AGG	AAG	GGA	GGG	720
	Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	
	225						230			235			240			

15	AAA	GCG	CTG	ACA	GCT	AAT	TTG	TGG	AAT	TGG	GTC	AAT	GAT	GCT	TGC	AGT	768
	Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	
	245						250				255						

	AGT	CTA	AGT	GGA	AAT	AAG	GAG	TCC	TCA	GGG	GAC	CGT	TGT	GCT	GGT	TCC	816
	Ser	Leu	'Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	
	260						265				270						

20	CAC	TCG	GCA	ACC	TCC	AGT	CAG	CAA	GAA	GTG	TGT	GAA	GGT	ATC	TTA	CTA	864
	His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	
	275						280				285						

25	ATG	ACT	CGG	GAG	GAG	AAG	ATG	GTT	CCA	GAA	GAC	GGT	GCT	GGT	GCA	TGT	912
	Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glut	Asp	Gly	Ala	Gly	Val	Cys	
	290						295				300						

30	GGG	CCT	GTG	TGT	GCG	GCA	GGT	GGG	CCC	TGG	GCA	GAA	GTC	AGA	GAT	TCT	960
	Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	
	305						310				315			320			

35	AGG	ACG	TTC	ACA	CTG	GTC	AGC	GAG	GTT	GAG	ACG	CAA	GGG	GAC	CTC	TCG	1008
	Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	
	325						330				335						

	AGG	AAG	ATT	CCC	ACA	GAG	GAT	GAG	TAC	ACG	GAC	CGG	CCC	TCG	CAG	CCT	1056
	Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro	
	340						345				350						

40	TCG	ACT	GGT	TCA	CTG	CTC	CTA	ATC	CAG	CAG	GGA	AGC	AAA	TCT	ATA	CCC	1104
	Ser	Thr	Gly	Ser	Leu	Leu	Leu		Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	
	355						360				365						

45	CCA	TTC	CAG	GAG	CCC	CTG	GAA	GTT	GGG	GAG	AAC	GAC	AGT	TTA	AGC	CAG	1152
	Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	
	370						375				380						

50	TGT	TTC	ACC	GGG	ACT	GAA	AGC	ACG	GTC	GAT	TCT	GAG	GGC	TGT	GAC	TTC	1200
	Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	
	385						390				395			400			

55	ACT	GAG	CCT	CCG	AGC	AGA	ACT	GAC	TCT	ATG	CCC	GTG	TCC	CCT	GAA	AAG	1248
	Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	
	405						410				415						

	CAC	CTG	ACA	AAA	GAA	ATA	GAA	GGT	GAC	AGT	TGC	CTC	CCC	TGG	GTG	GTC	1296
	His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	
	420						425				430						

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AGC TCC AAC TCA ACA GAT GGC TAC ACA GGC AGT GGG AAC ACT CCT GGG	1344
Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly	
435	440
	445

5 GAG GAC CAT GAA CCC TTT CCA GGG TCC CTG AAA TGT GGA CCA TTG CCC	1392
Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro	
450	455
	460

10 CAG TGT GCC TAC AGC ATG GGC TTT CCC AGT GAA GCA GCA GCC AGC ATG	1440
Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met	
465	470
	475
	480

15 GCA GAG GCG GGA GTA CGG CCC CAG GAC AGG GCT GAT GAG AGG GGA GCC	1488
Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala	
485	490
	495

20 TCA GGG TCC GGG AGC TCC CCC AGT GAC CAG CCA CCT GCC TCT GGG AAC	1536
Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn	
500	505
	510

25 GTG ACT GGA AAC AGT AAC TCC ACG TTC ATC TCT AGC GGG CAG GTG ATG	1584
Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met	
515	520
	525

30 AAC TTC AAG GGT GAC ATC ATC GTG GTG TAT GTC AGC CAG ACC TCG CAG	1632
Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln	
530	535
	540

35 GAG GGC CCG GGT TCC GCA GAG CCC GAG TCG GAG CCC GTG GGC CGC CCT	1680
Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro	
545	550
	555
	560

40 GTG CAG GAG GAG ACG CTG GCA CAC AGA GAC TCC TTT GCG GGC ACC GCG	1728
Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala	
565	570
	575

45 CCG CGC TTC CCC GAC GTC TGT GCC ACC GGG GCT GGG CTG CAG GAG CAG	1776
Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln	
580	585
	590

50 GGG GCA CCC CGG CAG AAG GAC GGG ACA TCG CGG CCG GTG CAG GAG CAG	1824
Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln	
595	600
	605

55 GGT GGG GCG CAG ACT TCA CTC CAT ACC CAG GGG TCC GGA CAA TGT GCA	1872
Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala	
610	615
	620

60 GAA TGA	1878
Glu	
625	

55 (2) INFORMATION FOR SEQ ID NO:15:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
5 1 5 10 15

Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
20 25 30

10 Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
35 40 45

Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
50 55 60

15 Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
65 70 75 80

20 Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
85 90 95

Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
100 105 110

25 Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
115 120 125

Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
130 135 140

30 Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
145 150 155 160

35 Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
165 170 175

Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
180 185 190

40 Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
195 200 205

Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
210 215 220

45 Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
225 230 235 240

50 Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
245 250 255

Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
260 265 270

55 His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
275 280 285

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
290 295 300

60

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Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
305 310 315 320

5 Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
340 345 350

10 Ser Thr Gly Ser Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
355 360 365

Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln
370 375 380

15 Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe
385 390 395 400

20 Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys
405 410 415

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
420 425 430

25 Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
450 455 460

30 Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
465 470 475 480

35 Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
500 505 510

40 Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
530 535 540

45 Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
545 550 555 560

50 Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln
580 585 590

55 Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln
595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
610 615 620

60

Glu
625

5 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
10 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

20 Gly Ser Thr Gly
20

25 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
30 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 Asp Tyr Lys Asp Glu
5

40 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
45 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

50 His His His His His
5

55 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
60 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

10 Arg

15

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